



## SEQUENCE LISTING

<110> Greene, Marianne E.  
Blumberg, Bruce E.

<120> Human Peroxisome Proliferator Activated Receptor Gamma: Compositions and Methods

<130> ARD

<160> 8

<170> PatentIn version 3.1

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<211> 1841

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (179)..(1603)

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ggtcggcctc gaggacaccg gagaggggcg ccacgccgcc gtggccgcag aaatgacc 178

atg gtt gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc 226  
Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser  
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tcc gtg gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc 274  
Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile  
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aag ccc ttc act act gtt gac ttc tcc agc att tct act cca cat tac 322  
Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr  
35 40 45

gaa gac att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag 370  
Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys  
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tat gac ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct 418  
Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro  
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gca tct cca cct tat tat tct gag aag act cag ctc tac aat aag cct 466  
Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro  
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cat gaa gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt 514  
His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys

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aga tgt gat ctt aac Arg Cys Asp Leu Asn 145	tgt cgg atc cac Cys Arg Ile His 150	aaa agt aga aat aaa tgt Lys Ser Arg Asn Lys Cys 155 160	658
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 Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu  
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Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr  
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Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys  
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Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro  
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Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro  
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His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys  
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Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly  
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Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp  
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Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys  
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Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn  
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Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu  
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Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe  
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Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr  
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Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly

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Glu Ala Val	Gln Glu Ile Thr Glu Tyr Ala Lys	Ser Ile Pro Gly Phe			
	290	295	300		
Val Asn Leu	Asp Leu Asn Asp Gln Val Thr	Leu Leu Lys Tyr Gly Val			
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His Glu Ile	Ile Tyr Thr Met Leu Ala Ser	Leu Met Asn Lys Asp Gly			
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Val Leu Ile	Ser Glu Gly Gln Gly Phe Met Thr Arg	Glu Phe Leu Lys			
	340	345	350		
Ser Leu Arg	Lys Pro Phe Gly Asp Phe Met Glu	Pro Lys Phe Glu Phe			
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Ala Val Lys	Phe Asn Ala Leu Glu Leu Asp Asp	Ser Asp Leu Ala Ile			
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Phe Ile Ala	Val Ile Ile Leu Ser Gly Asp Arg	Pro Gly Leu Leu Asn			
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Val Lys Pro	Ile Glu Asp Ile Gln Asp Asn Leu Leu	Gln Ala Leu Glu			
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Leu Gln Leu	Lys Leu Asn His Pro Glu Ser Ser	Gln Leu Phe Ala Lys			
	420	425	430		
Leu Leu Gln	Lys Met Thr Asp Leu Arg Gln Ile	Val Thr Glu His Val			
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Gln Leu Leu	Gln Val Ile Lys Lys Thr Glu Thr	Asp Met Ser Leu His			
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